

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

5

(A) NAME:

ASAT AG Applied Science & Technology

(B) STREET: Baarerstrasse 77

(C) CITY: Zug

(E) COUNTRY: Switzerland

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(F) POSTAL CODE: 6302

(ii) TITLE OF INVENTION: Recombinant antibodies

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(iii) NUMBER OF SEQUENCES: 30

(iv) COMPUTER-READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0,
Version #1.30 (EPO)

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(vi) ORIGINAL APPLICATION DATA:

(A) APPLICATION NUMBER: DE 19723904.8

(B) APPLICATION DATE: 06-JUN-1997

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(vi) ORIGINAL APPLICATION DATA:

(A) APPLICATION NUMBER: DE 19755227.7

(B) APPLICATION DATE: 12-DEC-1997

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

- 50 -

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) NOTATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAG GTG AAA CTG CTC GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG	48
Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu	
1 5 10 15	

ACC CTG TCC CTC AAC TGC ACT GTC TCT GGT CGC TCC ATC AGT GGT TAC	96
Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr	
20 25 30	

TCT TGG AGA TGG ATC CGG CAG TCT CCA GGG AAG GGA CTA GAG TGG ATT	144
Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile	
35 40 45	

GGG GAT ATC TCT TAT AGT GGG AGT ACC AAG TAC AAA CCC TCC CTC AGG	192
Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg	
50 55 60	

10 AGT CGA GTC ACC CTG TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG	240
Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu	
65 70 75 80	

AAG CTG AAT TCG GTG ACC GCT GCG GAC ACG GCC GTC TAT TAC TGT GCG	288
Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	

CGA GTC TTG CCC TTT GAC CCG ATC TCG ATG GAC GTC TGG GGC AAA GGG	336
Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly	
100 105 110	

ACC ACG GTC ACC GTC TCC TCA	357
Thr Thr Val Thr Val Ser Ser	
115	

(2) INFORMATION FOR SEQ ID NO: 2:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

- 51 -

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 20 25 30

Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 50 55 60

Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG TGG GTC
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val 48

120 125 130 135

ACC ATC TCT TGT TCT GGG AGC AGC TCC AAC ATC AGA AGT AAT CCT GTT
 Thr Ile Ser Cys Ser Gly Ser Ser Asn Ile Arg Ser Asn Pro Val 96

140 145 150

AGC TGG TAT CAC CAG GTC CCA GGC ACG GCC CCC AAA CTC CTC ATC TTT
 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe 144

155 160 165

GGT AGT CAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GCC TCC
 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser 192

170 175 180

AAG TCG GGC ACC TCC GCC TCC CTG GCC ATC CGT GGG CTC CAA TCT GGG
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly 240

185 190 195

- 52 -

GAT GCT GGT GAC TAT TAC TGT GCA ACA TGG GAT GAC GGC CTC AAT GGT
 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
 200 205 210 215

288

CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC
 Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
 220 225 230

333

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val
 1 5 10 15

Thr Ile Ser Cys Ser Gly Ser Ser Asn Ile Arg Ser Asn Pro Val
 20 25 30

Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
 35 40 45

Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
 65 70 75 80

Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
 85 90 95

Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 5:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

- 53 -

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 115 120 125	48
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 130 135 140	96
GCT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 145 150 155	144
GCA GTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 160 165 170 175	192
AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 180 185 190	240
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 195 200 205	288
GCG AGA GCG CTG GGG AGC TGG GGG GGT TGG GAC CAC TAC ATG GAC GTC Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val 210 215 220	336
TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 225 230	369

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val 100 105 110
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Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120
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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

10 (A) NAME/KEY: CDS
 (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG AGG GTC 48
 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 125 130 135

ACC ATC TCT TGT TCT GGA AGC AGC TCC AAC ATC GGA AGT AAT ACT GTA 96
 Thr Ile Ser Cys Ser Ser Gly Ser Asn Ile Gly Ser Asn Thr Val
 140 145 150 155

AAC TGG TAC CAG CAG CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT 144
 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 160 165 170

AGT AAT AAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GGC TCC 192
 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 175 180 185

AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC AGT GGG CTC CAG TCT GAG 240
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
 190 195 200

GAT GAG GCT GAT TAT TAC TGT GCA GCA TGG GAT GAC AGC CTG AAT GGT 288
 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
 205 210 215

TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT CAG CCC 333
 Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 220 225 230

15 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

- 55 -

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 1 5 10 15

Thr Ile Ser Cys Ser Gly Ser Ser Asn Ile Gly Ser Asn Thr Val
 20 25 30

Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 35 40 45

Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
 85 90 95

Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 9:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTT CAC CCC GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly	48
115 120 125	
TCC CTG AGA CTC TCT TGT GCA GCC TCT GGA TTT ACG TTT GAC AAC TTT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe	96
130 135 140	
GCC ATG AGC TGG GTC CGC CAG GCT CCA GGG AAG GGG CTG GAG TGG GTC Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	144
145 150 155	
TCA GGC ATT AGT GGT GGT CTT TTG ACA CAC TAC GCA GAC TCC GTG Ser Gly Ile Ser Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val	192
160 165 170 175	
AAG GGC CGG TTC ACC ATC TCC AGA AAC AAT TCC AGG AAC ACT GTA TAC Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr	240
180 185 190	
CTA CAA ATG AAC AGC CTG AGA GCC GAA GAC ACG GCC GTG TAT TAT TGT Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	288
195 200 205	

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GTG AGA GAT CTG GGC TAT AGA GTA CTT TCG ACT TTT ACT TTT GAT ATC 336
 Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile
 210 215 220

TGG GGC CAG GGG ACA AAG GTC ACC GTC TCT TCA 369
 Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
 225 230

(2) INFORMATION FOR SEQ ID NO: 10:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile
 100 105 110
 Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
 115 120

15 (2) INFORMATION FOR SEQ ID NO: 11:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTG GTG ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC	48
Val Val Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile	
125 130 135	
ACC ATC TCC TGC ACT GGA ACC AGC AGT GCT ATT GGG AAT TAT AAC TTT	96
Thr Ile Ser Cys Thr Gly Thr Ser Ala Ile Gly Asn Tyr Asn Phe	
140 145 150 155	
GTC CCC TGG TAC CAA CAG CAC CCA GGC AAA GCC CCC AAA CTC ATG ATT	144
Val Pro Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile	
160 165 170	
TAT GAG GGC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC	192
Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly	
175 180 185	
TCC AAG TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT	240
Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala	
190 195 200	
GAG GAC GAG GCT GAG TAT TAC TGC TGC TCA TAT GTT CAT AGT AGC ACT	288
Glu Asp Glu Ala Glu Tyr Tyr Cys Cys Ser Tyr Val His Ser Ser Thr	
205 210 215	
AAT TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT CAG CCC	336
Asn Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro	
220 225 230 235	
AAG GCT GCC CCC TCG GTC ACT CTG TTC CCA CCC TCC TCT	375
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser	
240 245	

5 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Val Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile	
1 5 10 15	
Thr Ile Ser Cys Thr Gly Thr Ser Ser Ala Ile Gly Asn Tyr Asn Phe	
20 25 30	
Val Pro Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile	
35 40 45	
Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly	
50 55 60	
Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala	
65 70 75 80	
Glu Asp Glu Ala Glu Tyr Tyr Cys Cys Ser Tyr Val His Ser Ser Thr	
85 90 95	

Asn Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CAG GTG AAA CTG CTC GAG TCA GGA CCA GGA CTG GTG AAG CCC TCG GAG Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu 130 135 140	48
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ACC CTG TCT CTC ACC TGC ACT GTC TCT GAT GTC TCC ATC AGA AGT CAT Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His 145 150 155	96
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TAC TGG AGT TGG CTC CGG CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile 160 165 170	144
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15 GGG TTT ATC TAT GAC GGT GCG AGA ACC AGG TTC AAC CCC TCC CTC AGG Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg 175 180 185	192
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AGT CGA GTC TCC CTT TCA ATG GAC CCA TCC AAG AAG CAG TTT TCC CTG Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu 190 195 200 205	240
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AAA CTG GGG TCT GTG ACC GCT GCG GAC TCG GCC GTC TAC TAC TGT GCG Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala 210 215 220	288
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AGA GAC GCG GAT GGA GAT GGC TTC AGC CCA TAC TAC TTT CCC TAC TGG Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp 225 230 235	336
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GGC CAG GGA ATC CCG GTC TCC GTC TCC TCG Gly Gln Gly Ile Pro Val Ser Val Ser Ser 240 245	366
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(2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His
 20 25 30

Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg
 50 55 60

Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu
 65 70 75 80

Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp
 100 105 110

Gly Gln Gly Ile Pro Val Ser Val Ser Ser
 115 120

5 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleotide

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

15 (B) LOCATION: 1..372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAC CCT GGG AGG 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val His Pro Gly Arg
 125 130 135

TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 140 145 150

ACT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 155 160 165 170

GCA CTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG 192
 Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 175 180 185

- 60 -

AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC	AAG AAC ACG CTA TAT	240
Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser	Lys Asn Thr Leu Tyr	
190	195	200
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT	GTG TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala	Val Tyr Tyr Cys	
205	210	215
GCG AAA GAT GGC CGG AGT GGG AGC TAC GCC AGG	TTC GAC GGT ATG GAC	336
Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg	Phe Asp Gly Met Asp	
220	225	230
GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA		372
Val Trp Gly Gln Gly Thr Thr Val Val Ser Ser		
235	240	245

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Gln Val Lys Leu Leu Glu Ser Gly Gly	Val Val His Pro Gly Arg		
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr	Phe Ser Ser Tyr		
20	25	30	
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys	Gly Leu Glu Trp Val		
35	40	45	
Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr	Tyr Ala Asp Ser Val		
50	55	60	
Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser	Lys Asn Thr Leu Tyr		
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	Ala Val Tyr Tyr Cys		
85	90	95	
Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg	Phe Asp Gly Met Asp		
100	105	110	
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120		

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..372

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CAG GTG AAA CTG CTC GAG TCT GGG GGA CGC TTG GTA CAG CCT GGC AGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Arg	
125 130 135 140	
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT GAT GAT TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
145 150 155	
GCC CTG CAC TGG GTC CGT CAA GCT CCA GGG AAG GGC CTG GAG TGG GTC	144
Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
160 165 170	
TCA GGT ATT AGT TGG GAT AGT GGT ACC ATA GGC TAT GCG GAC TCT GTG	192
Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val	
175 180 185	
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC TCC CTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
190 195 200	
CTG CAA ATG AAC AGT CTG AGA GCT GAG GAC ACG GCC TTG TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys	
205 210 215 220	
GTA AAA GAT ATG GGG TCT TCG GTA GTG GCT ACG TAC AAT GCT TTT GAT	336
Val Lys Asp Met Gly Ser Ser Val Val Ala Thr Tyr Asn Ala Phe Asp	
225 230 235	
ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA	372
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser	
240 245	

(2) INFORMATION FOR SEQ ID NO: 18:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
20 25 30	
Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
65 70 75 80	

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Val Lys Asp Met Gly Ser Ser Val Val Ala Thr Tyr Asn Ala Phe Asp
 100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 19:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA for mRNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE (E): AI-X2

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CAG GTG AAA CTG CTC GAG TCA GGC CCA GGA CTG GTG AAG CCT TCG GAG Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu	48
125 130 135 140	

ACC CTG TCC CTC ACC TGC ACT GTC TCT GGT GGC TCC TTC AGT ACT TAC Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr	96
145 150 155	

TAT TGG AGC TGG ATC CGG CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile	144
160 165 170	

GGG TAT ATC TAT TAC AGT GGG AAC ACC AAC TAC AAC CCC TCC CTC AAG Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys	192
175 180 185	

AGT CGA GCC ACC ATA TCA GTC GAC ACG TCC AAG AAC CAG TTC TCC CTG Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu	240
190 195 200	

AAG CTG AGC TCT GTT ACC GCC GCA GAC ACG GCC GTC TAT TAC TGT GCG Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala	288
205 210 215 220	

AGA CTG CGT AAC GAT GGC TGG AAT GAT GGC TTT GAT ATC TGG GGC CAA Arg Leu Arg Asn Asp Gly Trp Asn Asp Gly Phe Asp Ile Trp Gly Gln	336
225 230 235	

GGG ACA ATG GTC ACC GTC TCT TCA
Gly Thr Met Val Thr Val Ser Ser
240

360

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Arg Asn Asp Gly Trp Asn Asp Gly Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

25

(vii) IMMEDIATE SOURCE:

(B) CLONE (E): AI-B14

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 14

5

(B) MAP POSITION: q32.3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG	48
Gln Val Lys Leu Leu Ser Gly Gly Val Val Gln Pro Gly Arg	
125 130 135	

TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT GAC TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr	
140 145 150	

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
155 160 165	

GCA GCT ATA TCA TAT GAT GGA AGT AAC AAA TAC TAT GCA GAC TCC GTG	192
Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
170 175 180	

AAG GGC CGA TTC TCC ATC TCC AGA GAC AAT TCC AAC AAT ACG CTA TAT	240
Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr	
185 190 195 200	

CTG CAA ATG AGC ACC CTG AGA GCT GAG GAC ACG GCT GTC TAT TTC TGT	288
Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys	
205 210 215	

GCG AGA GAT TCG GAA ACG GCA ATA GCG GCA GCT GGA CGG TTT GAT ATC	336
Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Gly Arg Phe Asp Ile	
220 225 230	

TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA	369
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser	
235 240	

(2) INFORMATION FOR SEQ ID NO: 22:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

- 65 -

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Gly Arg Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 23:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

15 (vii) IMMEDIATE SOURCE:

- (B) CLONE (E): AI-B18

(viii) POSITION IN THE GENOME:

- (A) CHROMOSOME SEGMENT: 14
- (B) MAP POSITION: q32.3

20 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

- 66 -

CAG GTG AAA CTG CTC GAG TCT GGG GCT GAG GTG AAG AAG CCT GGG TCC Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 125 130 135	48
TCG GTG ATG GTC TCC TGC AAG GCT TCT GGA GGC ACC TTC AGC AGC CAT Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser His 140 145 150 155	96
ACT ATC AGC TGG GTG CCG CAG GCC CCT GGA CAA GGC CTT GAG TGG ATG Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 160 165 170	144
GGA GGG ATC ACC CCT ATC TTT GGT ACA GTG AAC TAC GCA CAG AAG TTC Gly Gly Ile Thr Pro Ile Phe Gly Thr Val Asn Tyr Ala Gln Lys Phe 175 180 185	192
CAG GGC AGA GTC ACC ATT ACC GCG GAC GAA CCC ACG AGC ACA GCC TAC Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Pro Thr Ser Thr Ala Tyr 190 195 200	240
ATG GAA CTG AGG AGC CTG ACA TCT GAC GAC TCG GGC ATC TAT TAC TGT Met Glu Leu Arg Ser Leu Thr Ser Asp Asp Ser Gly Ile Tyr Tyr Cys 205 210 215	288
GCG AGA GAA GAT GGC ACT ACA GTA CCA AGT CAA CCC CTT GAG TTC TGG Ala Arg Glu Asp Gly Thr Thr Val Pro Ser Gln Pro Leu Glu Phe Trp 220 225 230 235	336
GGC CAG GGA ACC CGG GTC ACC GTC TCC TCT Gly Gln Gly Thr Arg Val Thr Val Ser Ser 240 245	366

(2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15
Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser His 20 25 30
Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45
Gly Gly Ile Thr Pro Ile Phe Gly Thr Val Asn Tyr Ala Gln Lys Phe 50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Pro Thr Ser Thr Ala Tyr 65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Asp Asp Ser Gly Ile Tyr Tyr Cys 85 90 95
Ala Arg Glu Asp Gly Thr Thr Val Pro Ser Gln Pro Leu Glu Phe Trp 100 105 110
Gly Gln Gly Thr Arg Val Thr Val Ser Ser 115 120

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

15

(B) CLONE (E): AI-B24

(viii) POSITION IN THE GENOME:

20

(A) CHROMOSOME/SEGMENT: 14
 (B) MAP POSITION: q32.3

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..363

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
125 130 135	

TCC CTG AGA CTC TCC TGT TCA GCC TCT GGA TTC ACC TTC AAT AAA TAT	96
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr	
140 145 150	

GCA ATA CAC TGG GTC CGC CAG GCT CCA GGG AAG GGA CTG GAA TAT GTT	144
Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val	
155 160 165 170	

TCA GCT ATT AGT AGT AAT GGG GGT AAC ACA TAC TAC GCA GAC TCC GTG	192
Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val	
175 180 185	

AAG GGC AGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr	
190 195 200	

CTT CAA ATG AGC AGT CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
205 210 215	

GTT AGA GGA AGT GGG AGC TAC TTA GGA TAC TAC TTT GAC TAC TGG GGC	336
Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly	
220 225 230	

CAG GGA ACC CTG GTC ACC GTC TCC TCA
Gln Gly Thr Leu Val Thr Val Ser Ser
235 240

363

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 121 base pairs
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
35 40 45

Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

25

(vii) IMMEDIATE SOURCE:

(B) CLONE (E): AI-B24

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 22

5

(B) MAP POSITION: q11

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..366

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTG GTG ACT CAG CCA CCC TCG GTG TCA GTG GCT CCA AGA CAG ACG GCC	48
Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln Thr Ala	
125 130 135	
ACG ATT ACC TGT GGG GGA TAC AAG ATT GGA AGT AAA AGT GTC CAC TGG	96
Thr Ile Thr Cys Gly Gly Tyr Lys Ile Gly Ser Lys Ser Val His Trp	
140 145 150	
TAC CAA CAG AAG CCA GGC CAG GCC CCT GTC TTG GTC GTC TAT GAG GAT	144
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Glu Asp	
155 160 165	
TCC TAC CGG CCC TCA GAG ATC CCT GAG CGA TTC TCT GGC TCC AAC TCT	192
Ser Tyr Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser	
170 175 180 185	
GGG AAC ATG GCC ACC CTG ACC ATC ACC GGG GTC GAA GCC GGG GAT GAG	240
Gly Asn Met Ala Thr Leu Thr Ile Thr Gly Val Glu Ala Gly Asp Glu	
190 195 200	
GCC GAC TAC TAC TGT CAG GTG TGG GAT AAT ACT AAT GAT CAG ACG ATA	288
Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Thr Asn Asp Gln Thr Ile	
205 210 215	
TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC AAG GCT GCC	336
Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala	
220 225 230	
CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT	366
Pro Ser Val Thr Leu Phe Pro Pro Ser Ser	
235 240	

15 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

- 70 -

Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln Thr Ala
1 5 10 15

Thr Ile Thr Cys Gly Gly Tyr Lys Ile Gly Ser Lys Ser Val His Trp
20 25 30

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Glu Asp
35 40 45

Ser Tyr Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
50 55 60

Gly Asn Met Ala Thr Leu Thr Ile Thr Gly Val Glu Ala Gly Asp Glu
65 70 75 80

Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Thr Asn Asp Gln Thr Ile
85 90 95

Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala
100 105 110

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

15 (vii) IMMEDIATE SOURCE:

- (B) CLONE (E): AI-B38

(viii) POSITION IN THE GENOME:

- (A) CHROMOSOME/SEGMENT: 14

20 (B) MAP POSITION: q32.3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CAG GTG AAA CTG CTC GAG TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC 48
 Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 125 130 135
 TCA GTG AAG GTC TCC TGC AAG GTT TCC GGA TAC ACC CTC ACT GAA TTA 96
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
 140 145 150
 TCC ATG CAC TGG GTG CGA CAG GCT CCT GGA AAA GGG CTT GAG TGG ATG 144
 Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 155 160 165 170
 GGA GGT TTT GAT CCT GAA GAT GGT GAA ACA ATC TAC GCA CAG AAA TTC 192
 Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
 175 180 185
 CAG GGC AGA GTC ACC ATG ACC GAG GAC ACA TCT ACA GAC ACG GCC TAC 240
 Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 190 195 200
 ATG GAG CTG ACC AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT 288
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 205 210 215
 GAG ACA GGT CTG AGG TCG TAC AAC TAT GGT CGT AAC CTT GAC TAT TGG 336
 Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp
 220 225 230
 GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA 366
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 235 240

(2) INFORMATION FOR SEQ ID NO: 30:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
 20 25 30
 Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp
 100 105 110

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Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

Sub
a
7